

**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/663,618A**

1814

DATE: 06/16/97
TIME: 19:27:17

INPUT SET: S18386.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/663,618A**

DATE: 06/16/97
TIME: 19:27:20

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47
48      (ii) MOLECULE TYPE: cDNA
49
50      (ix) FEATURE:
51          (A) NAME/KEY: CDS
52          (B) LOCATION: 2..1399
53
54      (ix) FEATURE:
55          (A) NAME/KEY: mat_peptide
56          (B) LOCATION: 65..1399
57
58      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60      C ATG GTG CGG TCT GTG GCC TGG GCA GGT TTC ATG GTC CTG CTG ATG      46
61      Met Val Arg Ser Val Ala Trp Ala Gly Phe Met Val Leu Leu Met
62      -21 -20           -15           -10
63
64      ATC CCA TGG GGC TCT GCT GCA AAA CTG GTC TGC TAC TTC ACC AAC TGG      94
65      Ile Pro Trp Gly Ser Ala Ala Lys Leu Val Cys Tyr Phe Thr Asn Trp
66      -5             1             5             10
67
68      GCC CAG TAC AGA CAG GGG GAG GCT CGC TTC CTG CCC AAG GAC TTG GAC      142
69      Ala Gln Tyr Arg Gln Gly Ala Arg Phe Leu Pro Lys Asp Leu Asp
70      15            20            25
71
72      CCC AGC CTT TGC ACC CAC CTC ATC TAC GCC TTC GCT GGC ATG ACC AAC      190
73      Pro Ser Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn
74      30            35            40
75
76      CAC CAG CTG AGC ACC ACT GAG TGG AAT GAC GAG ACT CTC TAC CAG GAG      238
77      His Gln Leu Ser Thr Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu
78      45            50            55
79
80      TTC AAT GGC CTG AAG AAG ATG AAT CCC AAG CTG AAG ACC CTG TTA GCC      286
81      Phe Asn Gly Leu Lys Lys Met Asn Pro Lys Leu Lys Thr Leu Leu Ala
82      60            65            70
83
84      ATC GGA GGC TGG AAT TTC GGC ACT CAG AAG TTC ACA GAT ATG GTA GCC      334
85      Ile Gly Gly Trp Asn Phe Gly Thr Gln Lys Phe Thr Asp Met Val Ala
86      75            80            85            90
87
88      ACG GCC AAC AAC CGT CAG ACC TTT GTC AAC TCG GCC ATC AGG TTT CTG      382
89      Thr Ala Asn Asn Arg Gln Thr Phe Val Asn Ser Ala Ile Arg Phe Leu
90      95            100           105
91
92      CGC AAA TAC AGC TTT GAC GGC CTT GAC CTT GAC TGG GAG TAC CCA GGA      430
93      Arg Lys Tyr Ser Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly
94      110           115           120
95
96      AGC CAG GGG AGC CCT GCC GTA GAC AAG GAG CGC TTC ACA ACC CTG GTA      478
97      Ser Gln Gly Ser Pro Ala Val Asp Lys Glu Arg Phe Thr Thr Leu Val
98      125           130           135
99

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100	CAG GAC TTG GCC AAT GCC TTC CAG CAG GAA GCC CAG ACC TCA GGG AAG	526
101	Gln Asp Leu Ala Asn Ala Phe Gln Gln Glu Ala Gln Thr Ser Gly Lys	
102	140 145 150	
103		
104	GAA CGC CTT CTT CTG AGT GCA GCG GTT CCA GCT GGG CAG ACC TAT GTG	574
105	Glu Arg Leu Leu Ser Ala Ala Val Pro Ala Gly Gln Thr Tyr Val	
106	155 160 165 170	
107		
108	GAT GCT GGA TAC GAG GTG GAC AAA ATC GCC CAG AAC CTG GAT TTT GTC	622
109	Asp Ala Gly Tyr Glu Val Asp Lys Ile Ala Gln Asn Leu Asp Phe Val	
110	175 180 185	
111		
112	AAC CTT ATG GCC TAC GAC TTC CAT GGC TCT TGG GAG AAG GTC ACG GGA	670
113	Asn Leu Met Ala Tyr Asp Phe His Gly Ser Trp Glu Lys Val Thr Gly	
114	190 195 200	
115		
116	CAT AAC AGC CCC CTC TAC AAG AGG CAA GAA GAG AGT GGT GCA GCA GCC	718
117	His Asn Ser Pro Leu Tyr Lys Arg Gln Glu Ser Gly Ala Ala Ala	
118	205 210 215	
119		
120	AGC CTC AAC GTG GAT GCT GCT GTG CAA CAG TGG CTG CAG AAG GGG ACC	766
121	Ser Leu Asn Val Asp Ala Ala Val Gln Gln Trp Leu Gln Lys Gly Thr	
122	220 225 230	
123		
124	CCT GCC AGC AAG CTG ATC CTT GGC ATG CCT ACC TAC GGA CGC TCC TTC	814
125	Pro Ala Ser Lys Leu Ile Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe	
126	235 240 245 250	
127		
128	ACA CTG GCC TCC TCA TCA GAC ACC AGA GTG GGG GCC CCA GCC ACA GGG	862
129	Thr Leu Ala Ser Ser Asp Thr Arg Val Gly Ala Pro Ala Thr Gly	
130	255 260 265	
131		
132	TCT GGC ACT CCA GGC CCC TTC ACC AAG GAA GGA GGG ATG CTG GCC TAC	910
133	Ser Gly Thr Pro Gly Pro Phe Thr Lys Glu Gly Gly Met Leu Ala Tyr	
134	270 275 280	
135		
136	TAT GAA GTC TGC TCC TGG AAG GGG GCC ACC AAA CAG AGA ATC CAG GAT	958
137	Tyr Glu Val Cys Ser Trp Lys Gly Ala Thr Lys Gln Arg Ile Gln Asp	
138	285 290 295	
139		
140	CAG AAG GTG CCC TAC ATC TTC CGG GAC AAC CAG TGG GTG GGC TTT GAT	1006
141	Gln Lys Val Pro Tyr Ile Phe Arg Asp Asn Gln Trp Val Gly Phe Asp	
142	300 305 310	
143		
144	GAT GTG GAG AGC TTC AAA ACC AAG GTC AGC TAT CTG AAG CAG AAG GGA	1054
145	Asp Val Glu Ser Phe Lys Thr Lys Val Ser Tyr Leu Lys Gln Lys Gly	
146	315 320 325 330	
147		
148	CTG GGC GGG GCC ATG GTC TGG GCA CTG GAC TTA GAT GAC TTT GGC GGC	1102
149	Leu Gly Gly Ala Met Val Trp Ala Leu Asp Leu Asp Asp Phe Ala Gly	
150	335 340 345	
151		
152	TTC TCC TGC AAC CAG GGC CGA TAC CCC CTC ATC CAG ACG CTA CGG CAG	1150

**RAW SEQUENCE LISTING
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153	Phe Ser Cys Asn Gln Gly Arg Tyr Pro Leu Ile Gln Thr Leu Arg Gln			
154	350	355	360	
155				
156	GAA CTG AGT CTT CCA TAC TTG CCT TCA GGC ACC CCA GAG CTT GAA GTT		1198	
157	Glu Leu Ser Leu Pro Tyr Leu Pro Ser Gly Thr Pro Glu Leu Glu Val			
158	365	370	375	
159				
160	CCA AAA CCA GGT CAG CCC TCT GAA CCT GAG CAT GGC CCC AGC CCT GGA		1246	
161	Pro Lys Pro Gly Gln Pro Ser Glu Pro Glu His Gly Pro Ser Pro Gly			
162	380	385	390	
163				
164	CAA GAC ACG TTC TGC CAG GGC AAA GCT GAT GGG CTC TAT CCC AAT CCT		1294	
165	Gln Asp Thr Phe Cys Gln Gly Lys Ala Asp Gly Leu Tyr Pro Asn Pro			
166	395	400	405	410
167				
168	CGG GAA CGG TCC AGC TTC TAC AGC TGT GCA GCG GGG CGG CTG TTC CAG		1342	
169	Arg Glu Arg Ser Ser Phe Tyr Ser Cys Ala Ala Gly Arg Leu Phe Gln			
170	415	420	425	
171				
172	CAA AGC TGC CCG ACA GGC CTG GTG TTC AGC AAC TCC TGC AAA TGC TGC		1390	
173	Gln Ser Cys Pro Thr Gly Leu Val Phe Ser Asn Ser Cys Lys Cys Cys			
174	430	435	440	
175				
176	ACC TGG AAT TGAGTCGCTA AAGCCCCCTCC AGTCCCAGCT TTGAGGCTGG		1439	
177	Thr Trp Asn			
178	445			
179				
180	GCCCAGGATC ACTCTACAGC CTGCCCTCCTG GGTTTTCCCT GGGGGCCGCA ATCTGGCTCC		1499	
181				
182	TGCAGGCCTT TCTGTGGTCT TCCTTTATCC AGGCTTTCTG CTCTCAGCCT TGCCTTCCTT		1559	
183				
184	TTTTCTGGGT CTCCTGGGCT GCCCCTTTCA CTTGCAAAAT AAATCTTTGG TTTGTGCCCC		1619	
185				
186	TCTTCCCCAAA AAAAAAAA		1636	
187				
188	(2) INFORMATION FOR SEQ ID NO:2:			
189				
190	(i) SEQUENCE CHARACTERISTICS:			
191	(A) LENGTH: 466 amino acids			
192	(B) TYPE: amino acid			
193	(D) TOPOLOGY: linear			
194				
195	(ii) MOLECULE TYPE: protein			
196				
197	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			
198				
199	Met Val Arg Ser Val Ala Trp Ala Gly Phe Met Val Leu Leu Met Ile			
200	-21 -20	-15	-10	
201				
202	Pro Trp Gly Ser Ala Ala Lys Leu Val Cys Tyr Phe Thr Asn Trp Ala			
203	-5	1	5	10
204				
205	Gln Tyr Arg Gln Gly Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp Pro			

RAW SEQUENCE LISTING
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206 15 20 25
207
208 Ser Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn His
209 30 35 40
210
211 Gln Leu Ser Thr Thr Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu Phe
212 45 50 55
213
214 Asn Gly Leu Lys Lys Met Asn Pro Lys Leu Lys Thr Leu Leu Ala Ile
215 60 65 70 75
216
217 Gly Gly Trp Asn Phe Gly Thr Gln Lys Phe Thr Asp Met Val Ala Thr
218 80 85 90
219
220 Ala Asn Asn Arg Gln Thr Phe Val Asn Ser Ala Ile Arg Phe Leu Arg
221 95 100 105
222
223 Lys Tyr Ser Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser
224 110 115 120
225
226 Gln Gly Ser Pro Ala Val Asp Lys Glu Arg Phe Thr Thr Leu Val Gln
227 125 130 135
228
229 Asp Leu Ala Asn Ala Phe Gln Gln Glu Ala Gln Thr Ser Gly Lys Glu
230 140 145 150 155
231
232 Arg Leu Leu Leu Ser Ala Ala Val Pro Ala Gly Gln Thr Tyr Val Asp
233 160 165 170
234
235 Ala Gly Tyr Glu Val Asp Lys Ile Ala Gln Asn Leu Asp Phe Val Asn
236 175 180 185
237
238 Leu Met Ala Tyr Asp Phe His Gly Ser Trp Glu Lys Val Thr Gly His
239 190 195 200
240
241 Asn Ser Pro Leu Tyr Lys Arg Gln Glu Glu Ser Gly Ala Ala Ala Ser
242 205 210 215
243
244 Leu Asn Val Asp Ala Ala Val Gln Gln Trp Leu Gln Lys Gly Thr Pro
245 220 225 230 235
246
247 Ala Ser Lys Leu Ile Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe Thr
248 240 245 250
249
250 Leu Ala Ser Ser Asp Thr Arg Val Gly Ala Pro Ala Thr Gly Ser
251 255 260 265
252
253 Gly Thr Pro Gly Pro Phe Thr Lys Glu Gly Gly Met Leu Ala Tyr Tyr
254 270 275 280
255
256 Glu Val Cys Ser Trp Lys Gly Ala Thr Lys Gln Arg Ile Gln Asp Gln
257 285 290 295
258

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**SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text